# RAW SEQUENCE LISTING ERROR REPORT
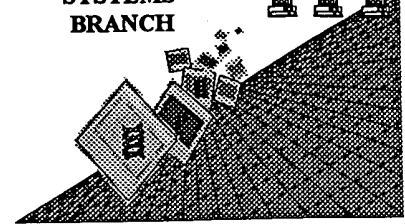
**BIOTECHNOLOGY SYSTEMS BRANCH**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: _09/177,387_

Art Unit / Team No. : _01 P6_

Date Processed by STIC: _11/3/98_

## THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

# Raw Sequence Listing Error Summary

ERROR DETECTED    SUGGESTED  CORRECTION

SERIAL NUMBER: _09/199,387_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

JAN 27 1999

2 _____ Wrapped Amines
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

GROUP 1800

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length.  This includes spaces.
All text must be visible on page.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and uses spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) features section that some may be missing.

7 _____ Wrong Designation
Sequence(s) _____ contain amino acid or nucleic acid designators which are not standard
representations as per the Sequence Rules (Please refer to paragraph 1.822)

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(I) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xl) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210>  sequence id number
<400>  sequence id number
000

10 _____ Use of N's or Xaa's (NEW RULES)
Use of N's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)
(Sec. 1.823 of new Sequence Rules)

13 _____ Wrong Format
File submitted was in the alphabetical heading format of the Old Sequence Rules.This is invalid since the
"Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Disclosures"
Federal Register Notice, Vol. 63, No. 104, June 1, 1998, p. 29620
applies to applications filed on or after July 1, 1998.

AKS-Biotechnology Systems Branch- 7/10/98

┌─────────────────────────────────────────────────────┐
│  This Raw Listing contains the General Information    │
│  Section and up to first 5 pages.                     │
└─────────────────────────────────────────────────────┘

_new format_

 1   <110> APPLICANT: Hartley, James L.
 2         Brasch, Michael A.
 3         Temple, Gary F.
 4         Fox, Donna K.
 5   <120> TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
 6         Recombination Sites
 7   <130> FILE REFERENCE: 0942.2850004
 8   <140> CURRENT APPLICATION NUMBER: US/09/177,387
 9   <141> CURRENT FILING DATE: 1998-10-23
10   <150> EARLIER APPLICATION NUMBER: US 60/065,930
11   <151> EARLIER FILING DATE: 1997-10-24            _Does Not Comply_
12   <160> NUMBER OF SEQ ID NOS: 60              _Corrected Diskette Needed_
13   <170> SOFTWARE: PatentIn Ver. 2.0
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25   <212> TYPE: DNA
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28   <223> OTHER INFORMATION: Description of Unknown Organism: recombination
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30   <400> SEQUENCE: 2                                              25
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34   <212> TYPE: DNA
35   <213> ORGANISM: Unknown
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38         products
39   <400> SEQUENCE: 3                    _item 10_                 25
40   gttcagcttt cktrtacnaa ctsgb
41   <210> SEQ ID NO 4
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44   <213> ORGANISM: Unknown

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W-->  40

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       63   <220> FEATURE:
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       81   <220> FEATURE:
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       84   <400> SEQUENCE: 8
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       89   <213> ORGANISM: Unknown
       90   <220> FEATURE:
       91   <223> OTHER INFORMATION: Description of Unknown Organism: recombination
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225    <220> FEATURE:
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228    <400> SEQUENCE: 24
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233    <213> ORGANISM: Artificial Sequence
234    <220> FEATURE:
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243    <220> FEATURE:
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**VERIFICATION SUMMARY**
PATENT APPLICATION **US/09/177,387**

DATE: 11/03/1998
TIME: 15:49:48

Input Set: **I177387.RAW**

| Line | ? | Error/Warning | Original Text |
|------|---|---------------|---------------|
| 22 | W | "N" or "Xaa" used: Feature required | rkycwgcttt yktrtacnaa stsgb |
| 31 | W | "N" or "Xaa" used: Feature required | agccwgcttt yktrtacnaa ctsgb |
| 40 | W | "N" or "Xaa" used: Feature required | gttcagcttt cktrtacnaa ctsgb |
| 49 | W | "N" or "Xaa" used: Feature required | agccwgcttt cktrtacnaa gtsgb |
| 58 | W | "N" or "Xaa" used: Feature required | gttcagcttt yktrtacnaa gtsgb |

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